Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/053,975_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ✓ Skipped Sequences
(NEW RULES)

Sequence(s) 3 missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 01/22/2003
PATENT APPLICATION: **US/10/053,975**   TIME: 15:47:59

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01222003\J053975.raw**

```
    4 <110> APPLICANT: LI, LIMIN
    5        COHEN, STANLEY N.
    7 <120> TITLE OF INVENTION: " Mammalian Tumor Susceptibility Gene
    8        Products and Their Uses"
   11 <130> FILE REFERENCE: STAN-216
   13 <140> CURRENT APPLICATION NUMBER: US 10/053,975
C--> 14 <141> CURRENT FILING DATE: 2003-01-10
   16 <150> PRIOR APPLICATION NUMBER: US 60/262,763
   17 <151> PRIOR FILING DATE: 2001-01-19
   19 <160> NUMBER OF SEQ ID NOS: 5
   21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
   23 <210> SEQ ID NO: 1
   24 <211> LENGTH: 390
   25 <212> TYPE: PRT
   26 <213> ORGANISM: Homo sapiens
   28 <400> SEQUENCE: 1
   29 Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
   30  1               5                  10                  15
   31 Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
   32             20                  25                  30
   33 Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
   34         35                  40                  45
   35 Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
   36     50                  55                  60
   37 Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
   38 65                  70                  75                  80
   39 Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
   40             85                  90                  95
   41 Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
   42             100                 105                 110
   43 Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
   44         115                 120                 125
   45 Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
   46     130                 135                 140
   47 Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
   48 145                 150                 155                 160
   49 Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
   50             165                 170                 175
   51 Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
   52         180                 185                 190
   53 Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
   54         195                 200                 205
   55 Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
```

**Does Not Comply
Corrected Diskette Needed**

P.2

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01222003\J053975.raw**

```
56      210                    215                    220
57 Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
58 225                    230                235                240
59 Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
60                245                250                255
61 Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
62                260                265                270
63 Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
64            275                280                285
65 Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys
66      290                295                300
67 Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro
68 305                    310                315                320
69 Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn
70                325                330                335
71 Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly
72            340                345                350
73 Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg
74            355                360                365
75 Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
76      370                375                380
77 Gly Leu Ser Asp Leu Tyr
78 385                390
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 10
83 <212> TYPE: PRT
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: hemagglutinin
89 <400> SEQUENCE: 2
90 Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
91 1               5               10
94 <210> SEQ ID NO: 3
96 <220> FEATURE:
97 <223> OTHER INFORMATION: FLAG
99 <400> SEQUENCE: 3
100 000
102 <210> SEQ ID NO: 4
103 <211> LENGTH: 11
104 <212> TYPE: PRT
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: c-myc
110 <400> SEQUENCE: 4
111 Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
112 1               5               10
115 <210> SEQ ID NO: 5
116 <211> LENGTH: 8
117 <212> TYPE: PRT
```

delete Please use format shown in item 8 of Error Summary Sheet.

W-->

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/053,975**

DATE: 01/22/2003
TIME: 15:47:59

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01222003\J053975.raw**

```
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 5
121 Tyr Pro Tyr Asp Val Pro Asp Tyr
122  1               5
```

VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/053,975**

DATE: 01/22/2003

TIME: 15:48:00

Input Set : **D:\seqlist.txt**

Output Set: **N:\CRF4\01222003\J053975.raw**

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:100 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (3) SEQUENCE:

STATISTICS SUMMARY
PATENT APPLICATION: **US/10/053,975**

DATE: 01/22/2003
TIME: 15:48:00

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01222003\J053975.raw**

Application Serial Number: US/10/053,975
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 01-10-2003
Art Unit: OIPE
Software Application: FastSEQ
Total Number of Sequences: 5
Total Nucleotides: 0
Total Amino Acids: 419
Number of Errors: 0
Number of Warnings: 1
Number of Corrections: 1

MESSAGE SUMMARY

271 C: 1 (Current Filing Date differs)
300 W: 1 ((50) Intentionally skipped Sequence)